

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/545,334

DATE: 05/02/2000

TIME: 13:22:40

Input Set : A:\0803.SEQLIST.txt

Output Set: N:\CRF3\050200\I545334.raw

ENTERED

4 <110> APPLICANT: Zinselmeier, Chris
 5 Habben, Jeff
 6 Tomes, Dwight
 8 <120> TITLE OF INVENTION: Regulated Expression of Genes in Plant
 9 Seeds
 11 <130> FILE REFERENCE: 0803p
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/545,334
 C--> 13 <141> CURRENT FILING DATE: 2000-04-07
 13 <160> NUMBER OF SEQ ID NOS: 12
 15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1608
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Zea mays
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)...(1605)
 27 <400> SEQUENCE: 1
 28 atg gcg gtg gtt tat tac ctg ctg ctg gcc ggg ctg atc gcc tgc tct 48
 29 Met Ala Val Val Tyr Tyr Leu Leu Ala Gly Leu Ile Ala Cys Ser
 30 1 5 10 15
 32 cat gca cta gcg gca ggc acg ctt gcg ctc gga gaa gat cgc ggc cgt 96
 33 His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg
 34 20 25 30
 36 ccc tgg cca gcc ttc ctc gcc gcg ctg gcc ttg gac ggc aag ctc cgg 144
 37 Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg
 38 35 40 45
 40 acc gac agc aac gcg acg gcg gcg gcc tcg acg gac ttc ggc aac atc 192
 41 Thr Asp Ser Asn Ala Thr Ala Ala Ala Ser Thr Asp Phe Gly Asn Ile
 42 50 55 60
 44 acg tcg gcg ctc ccg gcg gcg gtc cta tac ccg tcg tcc acg ggc gac 240
 45 Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp
 46 65 70 75
 48 ctg gtg gcg ctg ctg agc gcg gcc aac tcc acc ccg ggg tgg ccc tac 288
 49 Leu Val Ala Leu Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr
 50 85 90 95
 52 acc atc gcg ttc cgc ggc cgc ggc cac tcc ctc atg ggc cag gcc ttc 336
 53 Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe
 54 100 105 110
 56 gcc ccc ggc ggg gtg gtc gtc aac atg gcg tcc ctg ggc gac gcc gcc 384
 57 Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala
 58 115 120 125
 60 gcc gcc gcg ccg ccg cgc gtc aac gtg tcc gcg gac ggc cgc tac gtg 432
 61 Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val
 62 130 135 140
 64 gac gcc ggc ggc gag cag gtg tgg atc gac gtg ctg cgc gcg tct ctg 480
 65 Asp Ala Gly Gly Glu Gln Val Trp Ile Asp Val Leu Arg Ala Ser Leu

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 JUN 30 2000
 TECH CENTER 1600/2900

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66 145          150          155          160
68 gcg cgc ggc gtg gcg ccg cgc tcc tgg acc gac tac ctc tac ctc acc 528
69 Ala Arg Gly Val Ala Pro Arg Ser Trp Thr Asp Tyr Leu Tyr Leu Thr
70          165          170          175
72 gtc ggc ggc acg ctg tcc aac gca ggc atc agc ggc cag gcg ttc cgc
73 Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ala Phe Arg 576
74          180          185          190
76 cac ggc cca cag ata tct aac gtg ctg gag atg gac gtt atc acc ggc
77 His Gly Pro Gln Ile Ser Asn Val Leu Glu Met Asp Val Ile Thr Gly 624
78          195          200          205
80 cat ggg gag atg gtg acg tgc tcc aag cag ctg aac gcg gac ctg ttc
81 His Gly Glu Met Val Thr Cys Ser Lys Gln Leu Asn Ala Asp Leu Phe 672
82          210          215          220
84 gac gcc gtc ctg ggc ggg ctg ggg cag ttc gga gtg atc acc cgg gcc
85 Asp Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala 720
86          225          230          235
88 cgg atc gcg gtg gag ccg gcg ccg gcg cgg gcg cgg tgg gtg cgg ctc
89 Arg Ile Ala Val Glu Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Leu 768
90          245          250          255
92 gtg tac acc gac ttc gcg gcg ttc agc gcc gac cag gag cgg ctg acc
93 Val Tyr Thr Asp Phe Ala Ala Phe Ser Ala Asp Gln Glu Arg Leu Thr 816
94          260          265          270
96 gcc ccg cgg ccc ggc ggc ggc ggc gcg tcg ttc gcc ccg atg agc tac
97 Ala Pro Arg Pro Gly Gly Gly Ala Ser Phe Gly Pro Met Ser Tyr 864
98          275          280          285
100 gtg gaa ggg tcg gtg ttc gtg aac cag agc ctg gcg acc gac ctg gcg
101 Val Glu Gly Ser Val Phe Val Asn Gln Ser Leu Ala Thr Asp Leu Ala 912
102          290          295          300
104 aac acg ggg ttc ttc acc gac gcc gac gtc gcc cgg atc gtc gcg ctc
105 Asn Thr Gly Phe Phe Thr Asp Ala Asp Val Ala Arg Ile Val Ala Leu 960
106          305          310          315
108 gcc ggg gag cgg aac gcc acc acc gtg tac agc atc gag gcc acg ctc
109 Ala Gly Glu Arg Asn Ala Thr Thr Val Tyr Ser Ile Glu Ala Thr Leu 1008
110          325          330          335
112 aac tac gac aac gcc acg gcg gcg gcg gcg gtg gac cag gag ctc gcg
113 Asn Tyr Asp Asn Ala Thr Ala Ala Ala Ala Val Asp Gln Glu Leu Ala 1056
114          340          345          350
116 tcc gtg ctg ggc acg ctg agc tac gtg gaa ggg ttc gcg ttc cag cgc
117 Ser Val Leu Gly Thr Leu Ser Tyr Val Glu Gly Phe Ala Phe Gln Arg 1104
118          355          360          365
120 gac gtg tcc tac acg gcg ttc ctt gac cgg gtg cac ggc gag gag gtg
121 Asp Val Ser Tyr Thr Ala Phe Leu Asp Arg Val His Gly Glu Glu Val 1152
122          370          375          380
124 gcg ctc aac aag ctg ggg ctg tgg cgg gtg ccg cac ccg tgg ctc aac
125 Ala Leu Asn Lys Leu Gly Leu Trp Arg Val Pro His Pro Trp Leu Asn 1200
126          385          390          395
128 atg ttc gtg ccg cgc tcg cgc atc gcc gac ttc gac cgc ggc gtc ttc
129 Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe 1248
130          405          410          415

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132 aag ggc atc ttg cag ggc acc gac atc gtc ggc ccg ctc atc gtc tac
133 Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr 1296
134 420 425
136 ccc ctc aac aaa tcc atg tgg gac gac ggc atg tcg gcg gcg acg ccg
137 Pro Leu Asn Lys Ser Met Trp Asp Gly Met Ser Ala Ala Thr Pro 1344
138 435 440
140 tcg gag gac gtg ttc tac gcg gtg tcg ctg ctc ttc tcg tcg gtg gcg
141 Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala 1392
142 450 455
144 ccc aac gac ctg gcg agg ctg cag gag cag aac agg agg atc ctg cgc
145 Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg 1440
146 465 470
148 ttc tgc gac ctc gcc ggg atc cag tac aag acc tac ctg gcg cgg cac
149 Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His 1488
150 485 490
152 acg gac cgc agt gac tgg gtc cgc cac ttc ggc gcc gcc gag tgg aat
153 Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn 1536
154 500 505
156 cgc ttc gtg gag atg aag aac aag tac gac ccc aag agg ctg ctc tcc
157 Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser 1584
158 515 520
160 ccc ggc cag gac atc ttc aac tga
161 Pro Gly Gln Asp Ile Phe Asn 1608
162 530 535
165 <210> SEQ ID NO: 2
166 <211> LENGTH: 535
167 <212> TYPE: PRT
168 <213> ORGANISM: Zea mays
170 <400> SEQUENCE: 2
171 Met Ala Val Val Tyr Leu Leu Leu Ala Gly Leu Ile Ala Cys Ser
172 1 5 10 15
173 His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg
174 20 25 30
175 Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg
176 35 40 45
177 Thr Asp Ser Asn Ala Thr Ala Ala Ala Ser Thr Asp Phe Gly Asn Ile
178 50 55 60
179 Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp
180 65 70 75 80
181 Leu Val Ala Leu Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr
182 85 90 95
183 Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe
184 100 105 110
185 Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala
186 115 120 125
187 Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val
188 130 135 140
189 Asp Ala Gly Gly Glu Gln Val Trp Ile Asp Val Leu Arg Ala Ser Leu
190 145 150 155 160

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191 Ala Arg Gly Val Ala Pro Arg Ser Trp Thr Asp Tyr Leu Tyr Leu Thr
192                               165                               170
193 Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ala Phe Arg
194                               180                               185
195 His Gly Pro Gln Ile Ser Asn Val Leu Glu Met Asp Val Ile Thr Gly
196                               195                               200
197 His Gly Glu Met Val Thr Cys Ser Lys Gln Leu Asn Ala Asp Leu Phe
198                               210                               215
199 Asp Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala
200                               225                               230
201 Arg Ile Ala Val Glu Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Leu
202                               245                               250
203 Val Tyr Thr Asp Phe Ala Ala Phe Ser Ala Asp Gln Glu Arg Leu Thr
204                               260                               265
205 Ala Pro Arg Pro Gly Gly Gly Gly Ala Ser Phe Gly Pro Met Ser Tyr
206                               275                               280
207 Val Glu Gly Ser Val Phe Val Asn Gln Ser Leu Ala Thr Asp Leu Ala
208                               290                               295
209 Asn Thr Gly Phe Phe Thr Asp Ala Asp Val Ala Arg Ile Val Ala Leu
210                               305                               310
211 Ala Gly Glu Arg Asn Ala Thr Thr Val Tyr Ser Ile Glu Ala Thr Leu
212                               325                               330
213 Asn Tyr Asp Asn Ala Thr Ala Ala Ala Val Asp Gln Glu Leu Ala
214                               340                               345
215 Ser Val Leu Gly Thr Leu Ser Tyr Val Glu Gly Phe Ala Phe Gln Arg
216                               355                               360
217 Asp Val Ser Tyr Thr Ala Phe Leu Asp Arg Val His Gly Glu Glu Val
218                               370                               375
219 Ala Leu Asn Lys Leu Gly Leu Trp Arg Val Pro His Pro Trp Leu Asn
220                               385                               390
221 Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe
222                               405                               410
223 Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr
224                               420                               425
225 Pro Leu Asn Lys Ser Met Trp Asp Asp Gly Met Ser Ala Ala Thr Pro
226                               435                               440
227 Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala
228                               450                               455
229 Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg
230                               465                               470
231 Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His
232                               485                               490
233 Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn
234                               500                               505
235 Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser
236                               515                               520
237 Pro Gly Gln Asp Ile Phe Asn                               525
238                               530
240 <210> SEQ ID NO: 3                               535

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241 <211> LENGTH: 51
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium
 247 tumefaciens
 249 <400> SEQUENCE: 3
 250 caucacaucauc auggatccac caatggatct acgtctaatt ttcggtccaa c 51
 252 <210> SEQ ID NO: 4
 253 <211> LENGTH: 42
 254 <212> TYPE: DNA
 255 <213> ORGANISM: Artificial Sequence
 257 <220> FEATURE:
 258 <223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium
 259 tumefaciens
 261 <400> SEQUENCE: 4
 262 cuacuacuac uagttaactc acattcgaaa tgggtgctct tc 42
 264 <210> SEQ ID NO: 5
 265 <211> LENGTH: 29
 266 <212> TYPE: DNA
 267 <213> ORGANISM: Zea mays
 269 <400> SEQUENCE: 5
 270 catgccatgg cgggtggttta ttacctgct 42
 272 <210> SEQ ID NO: 6
 273 <211> LENGTH: 31
 274 <212> TYPE: DNA
 275 <213> ORGANISM: Zea mays
 277 <400> SEQUENCE: 6
 278 cgggacccctc atcatcagtt gaagatgtcc t 29
 280 <210> SEQ ID NO: 7
 281 <211> LENGTH: 5622
 282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: Promoter and terminator from Zea mays as found in
 287 Genbank Accession #S78780; gene from Agrobacterium
 288 tumefaciens as found in Molecular and General
 289 Genetics 216:388-394 (1989).
 291 <400> SEQUENCE: 7
 292 gctctagatt atataattta taagctaaac aaccgggcc taaagcacta tcgtatcacc 60
 293 tatctaaata agtcacggga gtttcgaacg tccacttcgt cgcacggaat tgcattgttc 120
 294 ttgttggaag catattcacg caatctccac acataaagg ttaggtataa acttacattt 180
 295 agctcagttt aattacagtc ttatttggat gcatatgtat ggttctcaat ccatataagt 240
 296 tagagtataa aataagttta aattttatct taattcactc caacatataat ggatctacaa 300
 297 tactcatgtg catccaaaca aactacttat attgagggtga atttggtaga aattaaacta 360
 298 acttacacac taagccaatc ttactatat taaagcacca gtttcaacga tcgtcccgcg 420
 299 tcaatattat taaaaaactc ctacatttct ttataatcaa cccgcactct tataatctct 480
 300 tctctactac tataataaga gagtttatgt acaaaataag gtgaaattat ctataagtgt 540
 301 tctggatatt ggttggtggc tcccatattc acacaaccta atcaatagaa aacatattgt 600

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/545,334

DATE: 05/02/2000
TIME: 13:22:41

Input Set : A:\0803.SEQLIST.txt

Output Set: N:\CRF3\050200\I545334.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date